```
==============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2009; month=3; day=24; hr=15; min=1; sec=14; ms=491; ]
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* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
Reviewer Comments:
<210> 8
<211> 139
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: partial
      sequence of pGEX2ThCD83ext

<400> 8
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Per the above sequence id# 8, please insert <220>, whenever numeric
identifiers <221>, <222> or <223> is present. Please correct the
remaining sequences showing similar errors. Please also correct <160>
response, there were a total of 13 sequences found not 12.

Ser Pro Asn Lys His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu

        195   200   205

Val
209

The above is a sample of invalid amino acid numbering also appearing in
sequence id# 13. Please number amino acids every 5th base.

```
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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Application No: 10535522   Version No: 2.0

Input Set:

Output Set:

Started:	2009-03-02 13:23:43.501
Finished:	2009-03-02 13:23:44.828
Elapsed:	0 hr(s) 0 min(s) 1 sec(s) 327 ms
Total Warnings:	8
Total Errors:	6
No. of SeqIDs Defined:	12
Actual SeqID Count:	13

Error code		Error Description
E	201	Mandatory field data missing in <140>
E	201	Mandatory field data missing in <141>
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
W	213	Artificial or Unknown found in <213> in SEQ ID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
W	213	Artificial or Unknown found in <213> in SEQ ID (11)
W	213	Artificial or Unknown found in <213> in SEQ ID (12)
E	323	Invalid/missing amino acid numbering SEQID (13)at Protein (209)
E	252	Calc# of Seq. differs from actual; 12 seqIds defined; count=13

SEQUENCE LISTING

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<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1)..(615)

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Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
 1   5   10   15

gct ccc gcg acg ccg gag gtg aag gtg gct tgc tcc gaa gat gtg gac   96
Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
            20   25   30

ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc   144
Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
        35   40   45

tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag   192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
    50   55   60

gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt   240
Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
 65   70   75   80

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac   288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
                85   90   95

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg   336
Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
            100   105   110

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga   384
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
        115   120   125

tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag   432
Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu

130   135   140

att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att   480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145   150   155   160

ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct   528
Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
                    165   170   175

aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag   576
Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
                    180   185   190

cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga   618
His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
                    195   200   205

<210> 2
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<213> Homo sapiens

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Met Ser Arg Gly Leu Gln Leu Leu Leu Leu Ser Cys Ala Tyr Ser Leu
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                    20   25   30

Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
                    35   40   45

Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
            50   55   60

Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
 65   70   75   80

Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
                            85   90   95

Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
                    100   105   110

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
            115   120   125

Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
            130   135   140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145   150   155   160

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
                    165   170   175

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
        180   185   190

His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
        195   200   205

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<211> 2051
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<213> Mus musculus
<220>
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            Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys
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gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct   97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala
            15   20   25

tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag   145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln
     30   35   40

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag   193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu
 45   50   55   60

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc   241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro
                65   70   75

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc   289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser
                80   85   90

tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac   337
Ser Gly Thr Tyr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn
                95   100   105

ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct   385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala
     110   115   120

aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc   433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe
125   130   135   140

tct ctg gtt gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt   481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe
                145   150   155

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gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa    529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu
            160               165               170

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg    577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val
        175               180               185


acc ctt cct aag aca gaa acg gta tgagtaggat ctccactggt ttttacaaag   631
Thr Leu Pro Lys Thr Glu Thr Val
        190               195

ccaagggcac atcagatcag tgtgcctgaa tgccacccgg acaagagaag aatgagctcc   691

atcctcagat ggcaaccttt ctttgaagtc cttcacctga cagtgggctc cacactactc   751

cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct   811

ctgtggctgt cagcttaatg tttcatgtgg ctatctggtc aacctcgtga gtgcttttca   871

gtcatctaca agctatggtg agatgcaggt gaagcagggt catgggaaat ttgaacactc   931

tgagctggcc ctgtgacaga ctcctgagga cagctgtcct ctcctacatc tgggatacat   991

ctctttgaat ttgtcctgtt tcgttgcacc agcccagatg tctcacatct ggcggaaatt  1051

gacaggccaa gctgtgagcc agtgggaaat atttagcaaa taatttccca gtgcgaaggt  1111

cctgctatta gtaaggagta ttatgtgtac atagaaatga gaggtcagtg aactattccc  1171

cagcagggcc ttttcatctg gaaaagacat ccacaaaagc agcaatacag agggatgcca  1231

catttatttt tttaatcttc atgtacttgt caaagaagaa ttttcatgt ttttcaaag    1291

aagtgtgttt ctttcctttt ttaaaatatg aaggtctagt tacatagcat tgctagctga  1351

caagcagcct gagagaagat ggagaatgtt cctcaaaata gggacagcaa gctagaagca  1411

ctgtacagtg ccctgctggg aagggcagac aatggactga gaaaccagaa gtctggccac  1471

aagattgtct gtatgattct ggacgagtca cttgtggttt tcactctctg gttagtaaac  1531

cagatagttt agtctgggtt gaatacaatg gatgtgaagt tgcttgggga aagctgaatg  1591

tagtgaatac attggcaact ctactgggct gttaccttgt tgatatccta gagttctgga  1651

gctgagcgaa tgcctgtcat atctcagctt gcccatcaat ccaaacacag gaggctacaa  1711

aaaggacatg agcatggtct tctgtgtgaa ctcctcctga gaaacgtgga gactggctca  1771

gcgctttgcg cttgaaggac taatcacaag ttcttgaaga tatggaccta ggggagctat  1831

tgcgccacga caggaggaag ttctcagatg ttgcattgat gtaacattgt tgcatttctt  1891

taatgagctg ggctccttcc tcatttgctt cccaaagaga ttttgtccca ctaatggtgt  1951
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gcccatcacc cacactatga aagtaaaagg gatgctgagc agatacagcg tgcttacctc 2011

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<212> PRT
<213> Mus musculus

<400> 4
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                20   25   30

Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
            35   40   45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
        50   55   60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
 65   70   75   80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
                85   90   95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
            100   105   110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
        115   120   125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
        130   135   140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145   150   155   160

Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
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Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
            180   185   190

Thr Glu Thr Val
        195

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<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: primer for CD83ext

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gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc   96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
        10   15   20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag   144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
    25   30   35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga   192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40   45   50   55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat   240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
                60   65   70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg   288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
            75   80   85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta   336

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
        90   95   100

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa   384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
    105   110   115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact   435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120   125   130

<210> 8
<211> 139
<212> PRT
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      sequence of pGEX2ThCD83ext

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Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
        10   15   20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
    25   30   35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40   45   50   55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
                60   65   70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
            75   80   85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
        90   95   100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
    105   110   115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120   125   130

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Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
                -5              -1   1                 5

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc    96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
         10              15                  20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag   144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
     25              30                  35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga   192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40              45                  50                  55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat   240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
                60                  65                  70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg   288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
             75                  80                  85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta   336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
             90                  95                 100

agt ggc aag gtg atc ttg aga gtg aca gga tcc cct gca cag cgt aaa   384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
    105                 110                 115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact   435
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
120                 125                 130


<210> 10
<211> 139
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: partial
      sequence of pGEX2ThCD83ext_mut129_CtoS

<400> 10
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
                -5              -1   1                 5

Val Lys Val Ala Cys Ser Glu Asp Val Asp Le
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